E. LAZAR

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000
TIME: 11:10:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

**Does Not Comply
Corrected Diskette Needed**

```
 4 <110> APPLICANT: Pier, Gerald B.
 6 <120> TITLE OF INVENTION: Methods and Products for Treating
 7        Pseudomonas Infection
 9 <130> FILE REFERENCE: B0801/7155 (HCL)
11 <140> CURRENT APPLICATION NUMBER: 09/405,735
12 <141> CURRENT FILING DATE: 1999-09-24
14 <150> PRIOR APPLICATION NUMBER: US 08/681,838
15 <151> PRIOR FILING DATE: 1996-07-29
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0


ERRORED SEQUENCES

21 <210> SEQ ID NO: 1
22 <211> LENGTH: 6129
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo Sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (133)...(4575)
30 <400> SEQUENCE: 1
31  aattggaagc aaatgacatc acagcaggtc agagaaaaag ggttgagcgg caggcaccca       60
32  gagtagtagg tctttggcat taggagcttg agcccagacg gccctagcag ggaccccagc      120
33  gcccgagaga cc atg cag agg tcg cct ctg gaa aag gcc agc gtt gtc tcc      171
34                Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser
35                 1               5                  10
37  aaa ctt ttt ttc agc tgg acc aga cca att ttg agg aaa gga tac aga      219
38  Lys Leu Phe Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg
39         15                  20                  25
41  cag cgc ctg gaa ttg tca gac ata tac caa atc cct tct gtt gat tct      267
42  Gln Arg Leu Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser
43     30                  35                  40                  45
45  gct gac aat cta tct gaa aaa ttg gaa aga gaa tgg gat aga gag ctg      315
46  Ala Asp Asn Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu
47                 50                  55                  60
49  gct tca aag aaa aat cct aaa ctc att aat gcc ctt cgg cga tgt ttt      363
50  Ala Ser Lys Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe
51                 65                  70                  75
53  ttc tgg aga ttt atg ttc tat gga atc ttt tta tat tta ggg gaa gtc      411
54  Phe Trp Arg Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val
55             80                  85                  90
57  acc aaa gca gta cag cct ctc tta ctg gga aga atc ata gct tcc tat      459
58  Thr Lys Ala Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr
59         95                 100                 105
61  gac ccg gat aac aag gag gaa cgc tct atc gcg att tat cta ggc ata      507
62  Asp Pro Asp Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile
```

```
63  110                     115                  120                   125
65  ggc tta tgc ctt ctc ttt att gtg agg aca ctg ctc cta cac cca gcc        555
66  Gly Leu Cys Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala
67                      130                  135                   140
69  att ttt ggc ctt cat cac att gga atg cag atg aga ata gct atg ttt        603
70  Ile Phe Gly Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe
71                      145                  150                   155
73  agt ttg att tat aag aag act tta aag ctg tca agc cgt gtt cta gat        651
74  Ser Leu Ile Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp
75                  160                  165                   170
77  aaa ata agt att gga caa ctt gtt agt ctc ctt tcc aac aac ctg aac        699
78  Lys Ile Ser Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn
79      175                  180                  185                      747
81  aaa ttt gat gaa gga ctt gca ttg gca cat ttc gtg tgg atc gct cct
82  Lys Phe Asp Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro
83  190                  195                  200                   205
85  ttg caa gtg gca ctc ctc atg ggg cta atc tgg gag ttg tta cag gcg        795
86  Leu Gln Val Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala
87                      210                  215                   220
89  tct gcc ttc tgt gga ctt ggt ttc ctg ata gtc ctt gcc ctt ttt cag       843
90  Ser Ala Phe Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln
91                  225                  230                   235
93  gct ggg cta ggg aga atg atg atg aag tac aga gat cag aga gct ggg        891
94  Ala Gly Leu Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly
95              240                  245                   250
97  aag atc agt gaa aga ctt gtg att acc tca gaa atg att gaa aat atc        939
98  Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile
99      255                  260                  265
101 caa tct gtt aag gca tac tgc tgg gaa gaa gca atg gaa aaa atg att       987
102 Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile
103 270                  275                  280                   285
105 gaa aac tta aga caa aca gaa ctg aaa ctg act cgg aag gca gcc tat       1035
106 Glu Asn Leu Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr
107                     290                  295                   300
109 gtg aga tac ttc aat agc tca gcc ttc ttc ttc tca ggg ttc ttt gtg       1083
110 Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val
111                 305                  310                   315
113 gtg ttt tta tct gtg ctt ccc tat gca cta atc aaa gga atc atc ctc       1131
114 Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu
115             320                  325                   330
117 cgg aaa ata ttc acc acc atc tca ttc tgc att gtt ctg cgc atg gcg       1179
118 Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala
119     335                  340                  345
121 gtc act cgg caa ttt ccc tgg gct gta caa aca tgg tat gac tct ctt       1227
122 Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu
123 350                  355                  360                   365
125 gga gca ata aac aaa ata cag gat ttc tta caa aag caa gaa tat aag       1275
126 Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys
127                 370                  375                   380
```

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

```
129  aca ttg gaa tat aac tta acg act aca gaa gta gtg atg gag aat gta   1323
130  Thr Leu Glu Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val
131              385                 390                 395
133  aca gcc ttc tgg gag gag gga ttt ggg gaa tta ttt gag aaa gca aaa   1371
134  Thr Ala Phe Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys
135              400                 405                 410
137  caa aac aat aac aat aga aaa act tct aat ggt gat gac agc ctc ttc   1419
138  Gln Asn Asn Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe
139      415                 420                 425
141  ttc agt aat ttc tca ctt ctt ggt act cct gtc ctg aaa gat att aat   1467
142  Phe Ser Asn Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn
143  430                 435                 440                 445
145  ttc aag ata gaa aga gga cag ttg ttg gcg gtt gct gga tcc act gga   1515
146  Phe Lys Ile Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly
147                  450                 455                 460
149  gca ggc aag act tca ctt cta atg atg att atg gga gaa ctg gag cct   1563
150  Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro
151                  465                 470                 475
153  tca gag ggt aaa att aag cac agt gga aga att tca ttc tgt tct cag   1611
154  Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln
155              480                 485                 490
157  ttt tcc tgg att atg cct ggc acc att aaa gaa aat atc atc ttt ggt   1659
158  Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly
159      495                 500                 505
161  gtt tcc tat gat gaa tat aga tac aga agc gtc atc aaa gca tgc caa   1707
162  Val Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln
163  510                 515                 520                 525
165  cta gaa gag gac atc tcc aag ttt gca gag aaa gac aat ata gtt ctt   1755
166  Leu Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu
167                  530                 535                 540
169  gga gaa ggt gga atc aca ctg agt gga ggt caa cga gca aga att tct   1803
170  Gly Glu Gly Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser
171                  545                 550                 555
173  tta gca aga gca gta tac aaa gat gct gat ttg tat tta tta gac tct   1851
174  Leu Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser
175              560                 565                 570
177  cct ttt gga tac cta gat gtt tta aca gaa aaa gaa ata ttt gaa agc   1899
178  Pro Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser
179      575                 580                 585
181  tgt gtc tgt aaa ctg atg gct aac aaa act agg att ttg gtc act tct   1947
182  Cys Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser
183  590                 595                 600                 605
185  aaa atg gaa cat tta aag aaa gct gac aaa ata tta att ttg aat gaa   1995
186  Lys Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu
187                  610                 615                 620
189  ggt agc agc tat ttt tat ggg aca ttt tca gaa ctc caa aat cta cag   2043
190  Gly Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln
191              625                 630                 635
193  cca gac ttt agc tca aaa ctc atg gga tgt gat tct ttc gac caa ttt   2091
```

```
194   Pro Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe
195       640                 645                 650
197   agt gca gaa aga aga aat tca atc cta act gag acc tta cac cgt ttc    2139
198   Ser Ala Glu Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe
199       655                 660                 665
201   tca tta gaa gga gat gct cct gtc tcc tgg aca gaa aca aaa aaa caa    2187
202   Ser Leu Glu Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln
203       670                 675                 680                 685
205   tct ttt aaa cag act gga gag ttt ggg gaa aaa agg aag aat tct att    2235
206   Ser Phe Lys Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile
207                   690                 695                 700
209   ctc aat cca atc aac tct ata cga aaa ttt tcc att gtg caa aag act    2283
210   Leu Asn Pro Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr
211           705                 710                 715
213   ccc tta caa atg aat ggc atc gaa gag gat tct gat gag cct tta gag    2331
214   Pro Leu Gln Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu
215       720                 725                 730
217   aga agg ctg tcc tta gta cca gat tct gag cag gga gag gcg ata ctg    2379
218   Arg Arg Leu Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu
219       735                 740                 745
221   cct cgc atc agc gtg atc agc act ggc ccc acg ctt cag gca cga agg    2427
222   Pro Arg Ile Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg
223   750                 755                 760                 765
225   agg cag tct gtc ctg aac ctg atg aca cac tca gtt aac caa ggt cag    2475
226   Arg Gln Ser Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln
227                   770                 775                 780
229   aac att cac cga aag aca aca gca tcc aca cga aaa gtg tca ctg gcc    2523
230   Asn Ile His Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala
231           785                 790                 795
233   cct cag gca aac ttg act gaa ctg gat ata tat tca aga agg tta tct    2571
234   Pro Gln Ala Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser
235       800                 805                 810
237   caa gaa act ggc ttg gaa ata agt gaa gaa att aac gaa gaa gac tta    2619
238   Gln Glu Thr Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu
239       815                 820                 825
241   aag gag tgc ctt ttt gat gat atg gag agc ata cca gca gtg act aca    2667
242   Lys Glu Cys Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr
243   830                 835                 840                 845
245   tgg aac aca tac ctt cga tat att act gtc cac aag agc tta att ttt    2715
246   Trp Asn Thr Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe
247                   850                 855                 860
249   gtg cta att tgg tgc tta gta att ttt ctg gca gag gtg gct gct tct    2763
250   Val Leu Ile Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser
251           865                 870                 875
253   ttg gtt gtg ctg tgg ctc ctt gga aac act cct ctt caa gac aaa ggg    2811
254   Leu Val Val Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly
255       880                 885                 890
257   aat agt act cat agt aga aat aac agc tat gca gtg att atc acc agc    2859
258   Asn Ser Thr His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser
```

RAW SEQUENCE LISTING   DATE: 05/09/2000
PATENT APPLICATION: US/09/405,735   TIME: 11:10:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

```
259        895                    900                 905
261   acc agt tcg tat tat gtg ttt tac att tac gtg gga gta gcc gac act    2907
262   Thr Ser Ser Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr
263   910                  915                920                 925
265   ttg ctt gct atg gga ttc ttc aga ggt cta cca ctg gtg cat act cta    2955
266   Leu Leu Ala Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu
267                  930                935                 940
269   atc aca gtg tcg aaa att tta cac cac aaa atg tta cat tct gtt ctt    3003
270   Ile Thr Val Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu
271                945                950                955
273   caa gca cct atg tca acc ctc aac acg ttg aaa gca ggt ggg att ctt    3051
274   Gln Ala Pro Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu
275                960                965                 970
277   aat aga ttc tcc aaa gat ata gca att ttg gat gac ctt ctg cct ctt    3099
278   Asn Arg Phe Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu
279        975                  980                985
281   acc ata ttt gac ttc atc cag ttg tta tta att gtg att gga gct ata    3147
282   Thr Ile Phe Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile
283   990                  995                1000                1005
285   gca gtt gtc gca gtt tta caa ccc tac atc ttt gtt gca aca gtg cca    3195
286   Ala Val Val Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro
287                1010                1015                1020
289   gtg ata gtg gct ttt att atg ttg aga gca tat ttc ctc caa acc tca    3243
290   Val Ile Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser
291                1025                1030                1035
293   cag caa ctc aaa caa ctg gaa tct gaa ggc agg agt cca att ttc act    3291
294   Gln Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr
295            1040                1045                1050
297   cat ctt gtt aca agc tta aaa gga cta tgg aca ctt cgt gcc ttc gga    3339
298   His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly
299       1055                1060                1065
301   cgg cag cct tac ttt gaa act ctg ttc cac aaa gct ctg aat tta cat    3387
302   Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His
W-->  303  1070                 1075                1080                1085
305   act gcc aac tgg ttc ttg tac ctg tca aca ctg cgc tgg ttc caa atg    3435
306   Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met
307                1090                1095                1100
309   aga ata gaa atg att ttt gtc atc ttc ttc att gct gtt acc ttc att    3483
310   Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile
311            1105                1110                1115
313   tcc att tta aca aca gga gaa gga gaa gga aga gtt ggt att atc ctg    3531
314   Ser Ile Leu Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu
315       1120                1125                1130
317   act tta gcc atg aat atc atg agt aca ttg cag tgg gct gta aac tcc    3579
318   Thr Leu Ala Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser
319       1135                1140                1145
321   agc ata gat gtg gat agc ttg atg cga tct gtg agc cga gtc ttt aag    3627
322   Ser Ile Asp Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys
W-->  323  1150                 1155                1160                1165
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000
TIME: 11:10:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

```
325  ttc att gac atg cca aca gaa ggt aaa cct acc aag tca acc aaa cca    3675
326  Phe Ile Asp Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro
327            1170                1175                1180
329  tac aag aat ggc caa ctc tcg aaa gtt atg att att gag aat tca cac    3723
330  Tyr Lys Asn Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His
331            1185                1190                1195
333  gtg aag aaa gat gac atc tgg ccc tca ggg ggc caa atg act gtc aaa    3771
334  Val Lys Lys Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys
335            1200                1205                1210
337  gat ctc aca gca aaa tac aca gaa ggt gga aat gcc ata tta gag aac    3819
338  Asp Leu Thr Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn
339       1215                1220                1225
341  att tcc ttc tca ata agt cct ggc cag agg gtg ggc ctc ttg gga aga    3867
342  Ile Ser Phe Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg
W--> 343  |230            1235                1240                1245
345  act gga tca ggg aag agt act ttg tta tca gct ttt ttg aga cta ctg    3915
346  Thr Gly Ser Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu
347            1250                1255                1260
349  aac act gaa gga gaa atc cag atc gat ggt gtg tct tgg gat tca ata    3963
350  Asn Thr Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile
351            1265                1270                1275
353  act ttg caa cag tgg agg aaa gcc ttt gga gtg ata cca cag aaa gta    4011
354  Thr Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val
355            1280                1285                1290
357  ttt att ttt tct gga aca ttt aga aaa aac ttg gat ccc tat gaa cag    4059
358  Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln
359       1295                1300                1305
361  tgg agt gat caa gaa ata tgg aaa gtt gca gat gag gtt ggg ctc aga    4107
362  Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg
W--> 363  |310            1315                1320                1325
365  tct gtg ata gaa cag ttt cct ggg aag ctt gac ttt gtc ctt gtg gat    4155
366  Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp
367            1330                1335                1340
369  ggg ggc tgt gtc cta agc cat ggc cac aag cag ttg atg tgc ttg gct    4203
370  Gly Gly Cys Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala
371            1345                1350                1355
373  aga tct gtt ctc agt aag gcg aag atc ttg ctg ctt gat gaa ccc agt    4251
374  Arg Ser Val Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser
375       1360                1365                1370
377  gct cat ttg gat cca gta aca tac caa ata att aga aga act cta aaa    4299
378  Ala His Leu Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys
379       1375                1380                1385
381  caa gca ttt gct gat tgc aca gta att ctc tgt gaa cac agg ata gaa    4347
382  Gln Ala Phe Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu
W--> 383  |390            1395                1400                1405
385  gca atg ctg gaa tgc caa caa ttt ttg gtc ata gaa gag aac aaa gtg    4395
386  Ala Met Leu Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val
387            1410                1415                1420
389  cgg cag tac gat tcc atc cag aaa ctg ctg aac gag agg agc ctc ttc    4443
```

RAW SEQUENCE LISTING   DATE: 05/09/2000
PATENT APPLICATION: US/09/405,735   TIME: 11:10:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

```
390   Arg Gln Tyr Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe
391        1425                1430                1435
393   cgg caa gcc atc agc ccc tcc gac agg gtg aag ctc ttt ccc cac cgg   4491
394   Arg Gln Ala Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg
395        1440                1445                1450
397   aac tca agc aag tgc aag tct aag ccc cag att gct gct ctg aaa gag   4539
398   Asn Ser Ser Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu
399        1455                1460                1465
401   gag aca gaa gaa gag gtg caa gat aca agg ctt tag agagcagcat        4585
402   Glu Thr Glu Glu Glu Val Gln Asp Thr Arg Leu   *
W-->  403  |470                1475                1480
405   aaatgttgac atgggacatt tgctcatgga attggagctc gtgggacagt cacctcatgg   4645
406   aattggagct cgtggaacag ttacctctgc ctcagaaaac aaggatgaat taagtttttt   4705
407   tttaaaaaag aaacatttgg taaggggaat tgaggacact gatatgggtc ttgataaatg   4765
408   gcttcctggc aatagtcaaa ttgtgtgaaa ggtacttcaa atccttgaag atttaccact   4825
409   tgtgttttgc aagccagatt ttcctgaaaa cccttgccat gtgctagtaa ttggaaaggc   4885
410   agctctaaat gtcaatcagc ctagttgatc agcttattgt ctagtgaaac tcgttaattt   4945
411   gtagtgttgg agaagaactg aaatcatact tcttagggtt atgattaagt aatgataact   5005
412   ggaaacttca gcggtttata taagcttgta ttccttttc tctcctctcc ccatgatgtt   5065
413   tagaaacaca actatattgt ttgctaagca ttccaactat ctcatttcca agcaagtatt   5125
414   agaataccac aggaaccaca agactgcaca tcaaaatatg ccccattcaa catctagtga   5185
415   gcagtcagga aagagaactt ccagatcctg gaaatcaggg ttagtattgt ccaggtctac   5245
416   caaaaatctc aatatttcag ataatcacaa tacatccctt acctgggaaa gggctgttat   5305
417   aatctttcac aggggacagg atggttccct tgatgaagaa gttgatatgc cttttcccaa   5365
418   ctccagaaag tgacaagctc acagaccttt gaactagagt ttagctggaa aagtatgtta   5425
419   gtgcaaattg tcacaggaca gcccttcttt ccacagaagc tccaggtaga gggtgtgtaa   5485
420   gtagataggc catgggcact gtgggtagac acacatgaag tccaagcatt tagatgtata   5545
421   ggttgatggt ggtatgtttt caggctagat gtatgtactt catgctgtct acactaagag   5605
422   agaatgagag acacactgaa gaagcaccaa tcatgaatta gttttatatg cttctgtttt   5665
423   ataattttgt gaagcaaaat ttttttctcta ggaaatattt attttaataa tgtttcaaac   5725
424   atatattaca atgctgtatt ttaaaagaat gattatgaat tacatttgta taaaataatt   5785
425   tttatatttg aaatattgac tttttatggc actagtattt ttatgaaata ttatgttaaa   5845
426   actgggacag gggagaacct agggtgatat taaccagggg ccatgaatca ccttttggtc   5905
427   tggagggaag ccttgggggct gatcgagttg ttgcccacag ctgtatgatt cccagccaga   5965
428   cacagcctct tagatgcagt tctgaagaag atggtaccac cagtctgact gtttccatca   6025
429   agggtacact gccttctcaa ctccaaactg actcttaaga agactgcatt atatttatta   6085
E-->  430   ctgtaagaaa atatcacttg tcaataaaat ccatacattt gtgt                 6129
432   <210> SEQ ID NO: 2
433   <211> LENGTH: 1480
434   <212> TYPE: PRT
435   <213> ORGANISM: Homo Sapiens
437   <400> SEQUENCE: 2
438   Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe
439   1                 5                  10                 15
440   Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu
441        20                 25                 30
442   Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn
443        35                 40                 45
444   Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000
TIME: 11:10:38

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

```
445          50                        55                        60
446    Lys Asn Pro Lys Leu Ile  Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg
447    65                       70                       75              80
448    Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala
449                        85                       90                   95
450    Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp
451                   100                      105                      110
452    Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys
453              115                      120                      125
454    Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly
455         130                      135                      140
456    Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile
457    145                      150                      155              160
458    Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser
459                   165                      170                      175
460    Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp
461                   180                      185                      190
462    Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val
463         195                      200                      205
464    Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe
465         210                      215                      220
466    Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu
467    225                      230                      235              240
468    Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser
469                   245                      250                      255
470    Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val
471                   260                      265                      270
472    Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu
473         275                      280                      285
474    Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr
475         290                      295                      300
476    Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu
477    305                      310                      315              320
478    Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile
479                   325                      330                      335
480    Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg
481                   340                      345                      350
482    Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile
483              355                      360                      365
484    Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu
485         370                      375                      380
486    Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe
487    385                      390                      395              400
488    Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn
489                   405                      410                      415
490    Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn
491              420                      425                      430
492    Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn Phe Lys Ile
493         435                      440                      445
```

```
494   Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly Ala Gly Lys
495       450                 455                 460
496   Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
497   465                 470                 475                 480
498   Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp
499                   485                 490                 495
500   Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr
501                   500                 505                 510
502   Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu
503           515                 520                 525
504   Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly
505       530                 535                 540
506   Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg
507   545                 550                 555                 560
508   Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly
509                   565                 570                 575
510   Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys
511                   580                 585                 590
512   Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu
513           595                 600                 605
514   His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly Ser Ser
515       610                 615                 620
516   Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe
517   625                 630                 635                 640
518   Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu
519                   645                 650                 655
520   Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu
521           660                 665                 670
522   Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys
523       675                 680                 685
524   Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro
525       690                 695                 700
526   Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln
527   705                 710                 715                 720
528   Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu
529                   725                 730                 735
530   Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile
531           740                 745                 750
532   Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser
533       755                 760                 765
534   Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His
535       770                 775                 780
536   Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala
537   785                 790                 795                 800
538   Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr
539                   805                 810                 815
540   Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys
541           820                 825                 830
542   Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp Asn Thr
```

```
                   835                    840                    845
543
544    Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile
545         850                    855                    860
546    Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val
547    865                    870                    875                    880
548    Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr
549                        885                    890                    895
550    His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr Ser Ser
551                 900                    905                    910
552    Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu Leu Ala
553             915                    920                    925
554    Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val
555         930                    935                    940
556    Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro
557    945                    950                    955                    960
558    Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe
559                        965                    970                    975
560    Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe
561                 980                    985                    990
562    Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val
563             995                    1000                   1005
564    Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile Val
565    1010                   1015                   1020
566    Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser Gln Gln Leu
E--> 567    1025                   1030                   1035                   1040
568    Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr His Leu Val
569                 1045                   1050                   1055
570    Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly Arg Gln Pro
571             1060                   1065                   1070
572    Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His Thr Ala Asn
573             1075                   1080                   1085
574    Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met Arg Ile Glu
575    1090                   1095                   1100
576    Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile Ser Ile Leu
E--> 577    1105                   1110                   1115                   1120
578    Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu Thr Leu Ala
579                 1125                   1130                   1135
580    Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser Ser Ile Asp
581             1140                   1145                   1150
582    Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys Phe Ile Asp
583    1155                   1160                   1165
584    Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn
585    1170                   1175                   1180
586    Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys
E--> 587    1185                   1190                   1195                   1200
588    Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu Thr
589                 1205                   1210                   1215
590    Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile Ser Phe
591             1220                   1225                   1230
```

```
592  Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg Thr Gly Ser
593       1235                    1240                      1245
594  Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr Glu
595       1250                    1255                      1260
596  Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr Leu Gln
E--> 597  1265                    1270                      1275         1280
598  Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val Phe Ile Phe
599       1285                    1290                      1295
600  Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln Trp Ser Asp
601       1300                    1305                      1310
602  Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg Ser Val Ile
603       1315                    1320                      1325
604  Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp Gly Gly Cys
605       1330                    1335                      1340
606  Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala Arg Ser Val
E--> 607  1345                    1350                      1355         1360
608  Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser Ala His Leu
609       1365                    1370                      1375
610  Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe
611       1380                    1385                      1390
612  Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu
613       1395                    1400                      1405
614  Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr
615       1410                    1415                      1420
616  Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala
E--> 617  1425                    1430                      1435         1440
618  Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser
619       1445                    1450                      1455
620  Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu
621       1460                    1465                      1470
622  Glu Glu Val Gln Asp Thr Arg Leu
623       1475                    1480
```

5/9/00

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/405,735

DATE: 05/09/2000
TIME: 11:10:39

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\05092000\I405735.raw

L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:430 M:254 E: (42) Number of Bases conflicts Running Total, LENGTH:Input:1 Counted:6129
L:567 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2